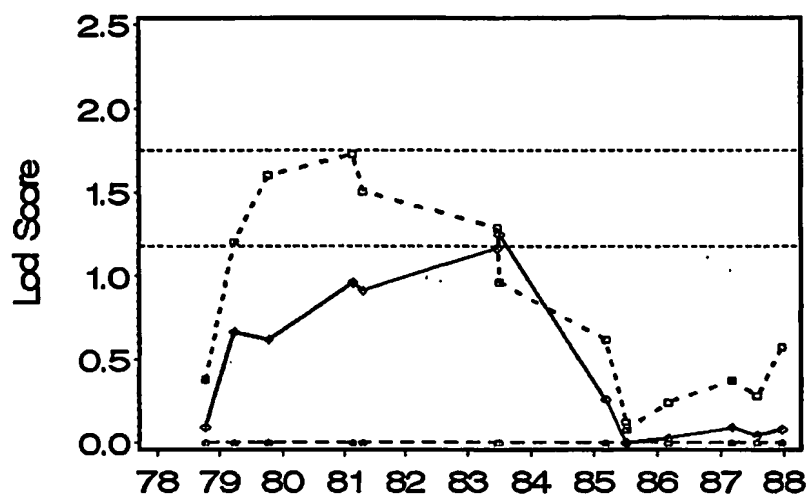


1/7

A



B

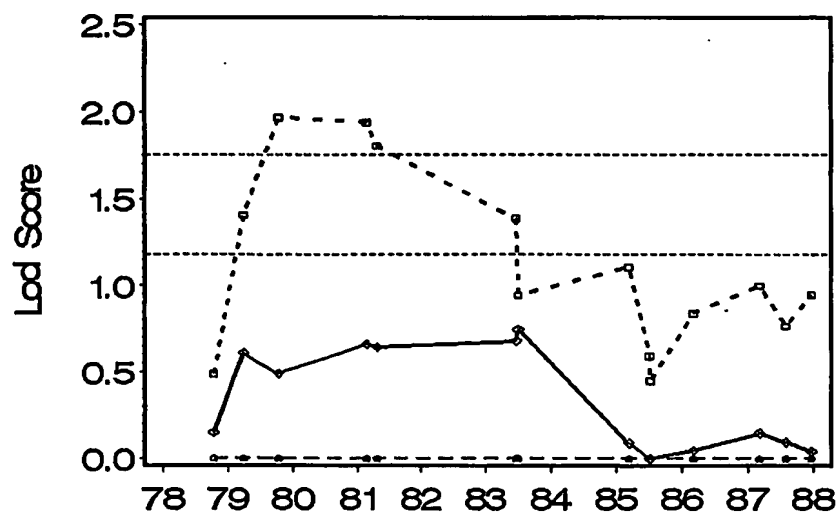
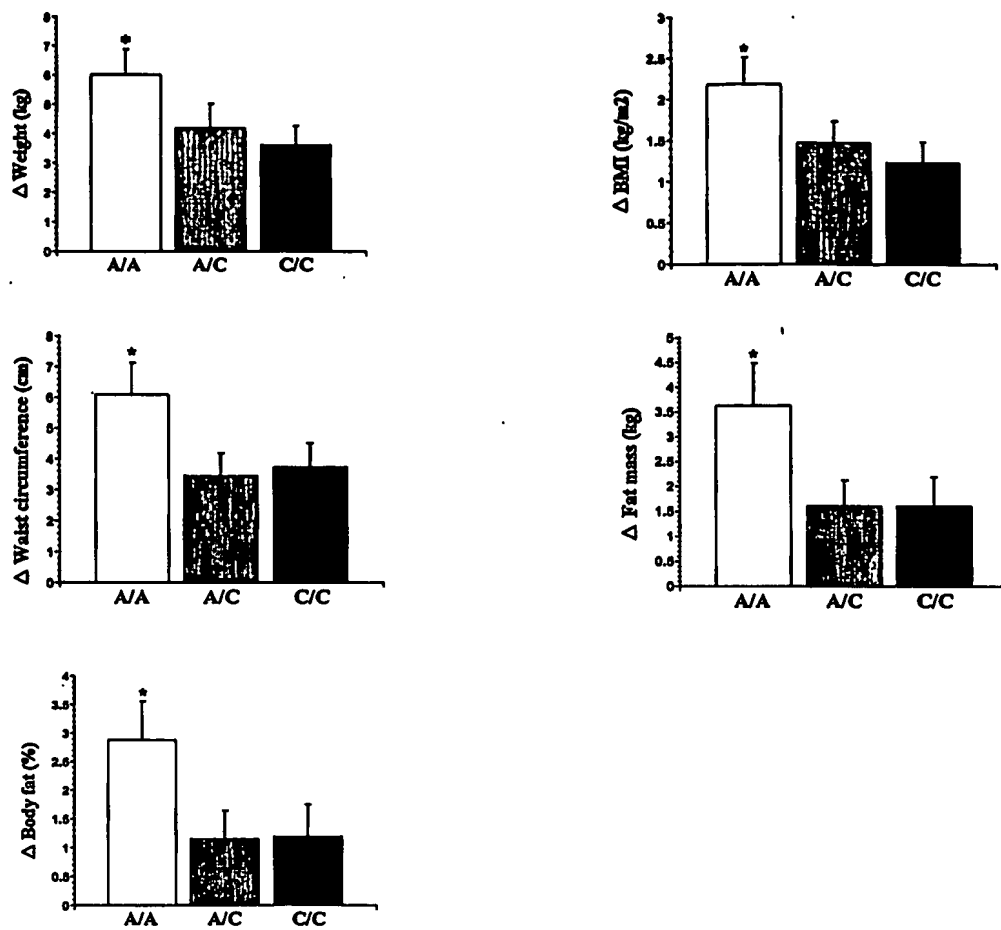


Fig. 1

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Fig. 2

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Homo sapiens

MARRAGGARMFGSLLLFALLAAGVAPLSWDLPEPRSRASKIRVHSRGNLWATGHFMGKKS 60

Mus musculus

MTRQAGSSWLLRGLLLFALFASGVAPFNWDLPEPRSRASKIRVHPRGNLWATGHFMGKKS 60

Homo sapiens

LEPSSPSPLGTAPHTSLRDQRLQLSHDLLGILLKKALGVSLSRPAPQIQYRRLVQILQK 121

Mus musculus

LEPPSLSLVGTAPPNTPRDQRLQLSHDLLRILLRKKALGMNFSGPAPPIQYRRLLEPLLQK 121

Fig. 3

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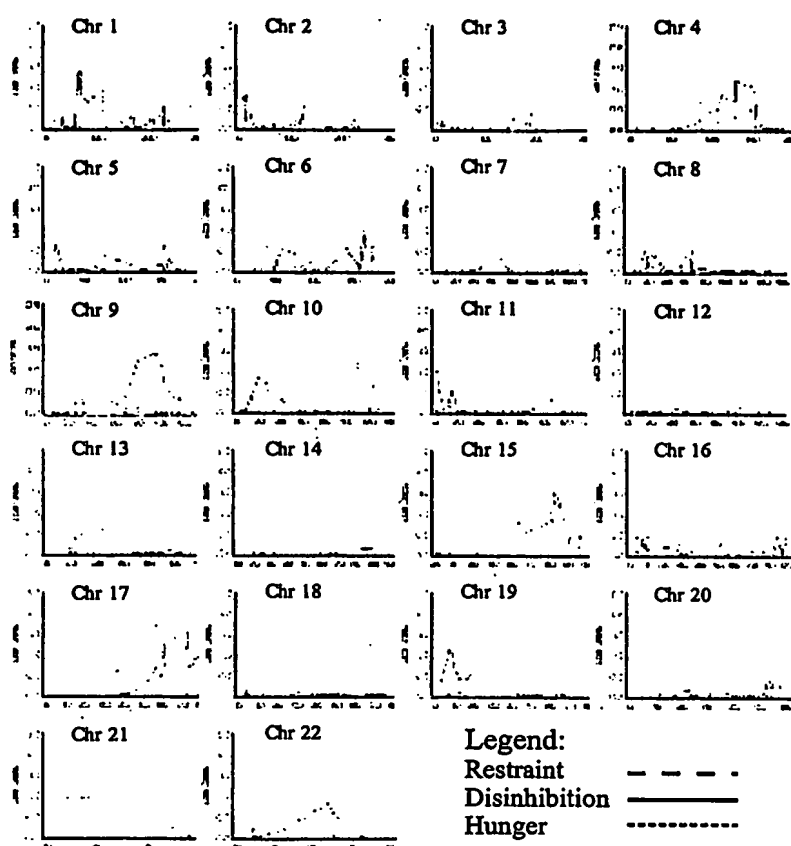


Fig. 4

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NMB_REF
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NMB_MUT
CTGTTACCCGGGAGGAGAGCTCTTCGCCCGACCTCTACCCTCATGAAGAGAGGCTCAGAG

NMB_REF
GGCTGAAAGTGCCTATTTGGCCGAAAGCCGTGGCAGAGTGGCAAGGCAGGGCCAGGGGAAAG 120
NMB_MUT
GGCTGAAAGTGCCTATTTGGCCGAAAGCCGTGGCAGAGTGGCAAGGCAGGGCCAGGGGAAAG

NMB_REF
CGGCTCCGCCCGGGGCCGGGGCCCTGTTTGGCCGGTGCCCGGTCCTTAGCCTGAAGGT 180
NMB_MUT
CGGCTCCGCCCGGGGCCGGGGCCCTGTTTGGCCGGTGCCCGGTCCTTAGCCTGAAGGT

NMB_REF
GGCGGGCTTCCGCCAGAAGCCCCTGGCGGAAGCGGTGCCCGCGTGCGGGCCAGAGTGTGG 240
NMB_MUT
GGCGGGCTTCCGCCAGAAGCCCCTGGCGGAAGCGGTGCCCGCGTGCGGGCCAGAGTGTGG

NMB_REF
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NMB_MUT
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NMB_REF
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NMB_MUT
TGGGGACGGCGGGGAGGGCGGCGGGCGGGGACGGCTCCGCTGCTCAGGGCAGGCTCC

NMB_REF
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NMB_MUT
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NMB_REF
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NMB_MUT
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NMB_REF
GGATGTTTCGGCAGCCTCCTGCTCTTCGCCCTGCTCGCTGCCGGCGTCGCCCCGCTCAGCT 540
NMB_MUT
GGATGTTTCGGCAGCCTCCTGCTCTTCGCCCTGCTCGCTGCCGGCGTCGCCCCGCTCAGCT

Fig. 5

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NMB_REF
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NMB_MUT
GGGATCTCCCGGAGCCCCGCAGCCGAGCCAGCAAGATCCGAGTGCACTCGCGAGGCAACC

NMB_REF
TCTGGGCCACCGGTAAGTCTTTGGGGACGGAGCAAGCAAGCGCCCCTCATCCAGTTCAGA 660
NMB_MUT
TCTGGGCCACCGGTAAGTCTTTGGGGACGGAGCAAGCAAGCGCCCCTCATCCAGTTCAGA

NMB_REF
CCCATTTCCTTCTCAACCCTCTGGCCGCTCCTCAGCCACGGACACTAGTGTCGGAGCAG 720
NMB_MUT
CCCATTTCCTTCTCAACCCTCTGGCCGCTCCTCAGCCACGGACACTAGTGTCGGAGCAG

NMB_REF
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NMB_MUT
GTGGAACACCGTGGGGCTCATCTAATTTAATAGATATGTACTTGAGACCCGGACAGGTCA

NMB_REF
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NMB_MUT
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NMB_REF
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NMB_MUT
ACTGCCAGCCGGTGCCCCCTTACCTTAGGCGAGACTTAACCGAATCTTCTAACCGCTGGTG

NMB_REF
TGTTTTTGCTGCACCTCCACTTTCCAGGCGCCTCTTCACTCTCCACTTCCTACCCTGCCC 960
NMB_MUT
TGTTTTTGCTGCACCTCCACTTTCCAGGCGCCTCTTCACTCTCCACTTCCTACCCTGCCC

NMB_REF
TTTTTCGTCCCTTGCCAAGCAGCCCACACAAGTAGCAGAGTTTCTCCCTGGCCCTGGAC 1020
NMB_MUT
TTTTTCGTCCCTTGCCAAGCAGCCCACACAAGTAGCAGAGTTTCTCCCTGGCCCTGGAC

NMB_REF
CATCCACCTTCCTGCCAGCTGTGCCATCCTCTCTACCTGTTTCAGGAAAAGCTGAGGGAG 1080
NMB_MUT
CATCCACCTTCCTGCCAGCTGTGCCATCCTCTCTACCTGTTTCAGGAAAAGCTGAGGGAG

Fig. 5 (cont')

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NMB_REF
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NMB_MUT
CAGGATTTGCCACCACCCAGACACCTTTGTGGCTCCTTGGTGAGGTGGAAGCACCAAGAG

NMB_REF
GAGGAAGGTTAAGTGTCTTCCCGCTACAAGAACGGAAACGTGGGAGAGATGAGGAACTTT 1200
NMB_MUT
GAGGAAGGTTAAGTGTCTTCCCGCTACAAGAACGGAAACGTGGGAGAGATGAGGAACTTT

NMB_REF
TCCTCTGAGGTAGGATCCTGGCTGCTTGACTTCCTTGTGCCTGGACACCTCCTTTCCAGG 1260
NMB_MUT
TCCTCTGAGGTAGGATCCTGGCTGCTTGACTTCCTTGTGCCTGGACACCTCCTTTCCAGG

NMB_REF
TCACTTCATGGGCAAGAAGAGTCTGGAGCCTTCCAGCCCATCCCCATTGGGGACAGCTCC 1320
NMB_MUT
TCACTTCATGGGCAAGAAGAGTCTGGAGCCTTCCAGCCCATCCCCATTGGGGACAGCTAC

NMB_REF
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NMB_MUT
CCAACCTCCCTGAGGGACCAGCGACTGCAGCTGAGTCATGATCTGCTCGGAATCCTCCT

NMB_REF
GCTAAAGAAGGCTCTGGGCGTGAGCCTCAGCCGCCCCGCACCCCAAATCCAGGTGAGCCG 1440
NMB_MUT
GCTAAAGAAGGCTCTGGGCGTGAGCCTCAGCCGCCCCGCACCCCAAATCCAGGTGAGCCG

NMB_REF
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NMB_MUT
GGCCCTGCTCCAATGTCAGGAGGGCCCAGCTGGGGCCATCCCCGGATCCTGCATGGAAG

NMB_REF
GAATTACCACCCAGTACTGTATTAGGGTGTGACTGTCTGACTAGGACATTATGGGTGTGG 1560
NMB_MUT
GAATTACCACCCAGTACTGTATTAGGGTGTGACTGTCTGACTAGGACATTATGGGTGTGG

NMB_REF
ACCCAGAAAGCCAGGTTTCCAGGCTTTCCCTCTTGAGGCAGAGCTCAAAGGAGGAACA 1620
NMB_MUT
ACCCAGAAAGCCAGGTTTCCAGGCTTTCCCTCTTGAGGCAGAGCTCAAAGGAGGAACA

Fig. 5 (cont')

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NMB_MUT
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NMB_REF
AGTTCCCCTGACTCATCACCCAGTCTAAAGTAACAGACTGGGATCATCAGCCTTTTGGAG 1740
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NMB_REF
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NMB_MUT
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NMB_REF
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NMB_MUT
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NMB_REF
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NMB_MUT
CCCAGAGAGGGAAAGAGAAAGTCAGCAGCCAAGACAGAGTCTGGACCTTGTTACCTGGAC

NMB_REF
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NMB_MUT
TGGAGCTCTTCCCATTCTCTCATCTGCCTCAGTATCCAGTGGTAGGGTTTAGCAACTTCA

NMB_REF
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NMB_MUT
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NMB_REF
GGATGTTTGGCAGCATCCCTGGTCTCTACATACTAGATGCCAGTAGCATCTTTCCCCCCC 2100
NMB_MUT
GGATGTTTGGCAGCATCCCTGGTCTCTACATACTAGATGCCAGTAGCATCTTTCCCCCCC

NMB_REF
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NMB_MUT
ATCAAGTTGTGACAACTGAAAAGACCTCCAGACATCACCAGATGTCTGCTGGGGGAGAGG

Fig. 5 (cont')

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NMB_MUT
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NMB_REF
AGCCAAGCTAGCCTCAAGGTATAGCCCCGCTGAGTGGCAACTCCTTCATTCCCTGCTCCT 2280
NMB_MUT
AGCCAAGCTAGCCTCAAGGTATAGCCCCGCTGAGTGGCAACTCCTTCATTCCCTGCTCCT

NMB_REF
GGTGCTGTCTTACTGCACACCACCCTCCCTGGTCTGCTGCTGTGTGCAGAAGGCAGTG 2340
NMB_MUT
GGTGCTGTCTTACTGCACACCACCCTCCCTGGTCTGCTGCTGTGTGCAGAAGGCAGTG

NMB_REF
TGATGTGGTAGAATGTGGGTTTTGACTACAACGTGCTGGGCTCATAACCTAGCTACTTAG 2400
NMB_MUT
TGATGTGGTAGAATGTGGGTTTTGACTACAACGTGCTGGGCTCATAACCTAGCTACTTAG

NMB_REF
TAGCTGTATGACCTTAGAAATGTCCCTTAACTTCTCTAAAGCCTCAATATTCTTCACCCA 2460
NMB_MUT
TAGCTGTATGACCTTAGAAATGTCCCTTAACTTCTCTAAAGCCTCAATATTCTTCACCCA

NMB_REF
TAAAATGAAGATAATAAGGCCCATCTCCCATTAATGAGACCATTTATGTCAAATGCTCA 2520
NMB_MUT
TAAAATGAAGATAATAAGGCCCATCTCCCATTAATGAGACCATTTATGTCAAATGCTCA

NMB_REF
GCATGGTGCCTGGCTCATAGACAGCCCTTAGTAGATGCGAGCTCTTATCAGTCTGTGAGC 2580
NMB_MUT
GCATGGTGCCTGGCTCATAGACAGCCCTTAGTAGATGCGAGCTCTTATCAGTCTGTGAGC

NMB_REF
TCCCTGGCGGCACCTGTTGTAGACTCGCCTTCATATCCCCCAGTGTGCCTAGCATATAGT 2640
NMB_MUT
TCCCTGGCGGCACCTGTTGTAGACTCGCCTTCATATCCCCCAGTGTGCCTAGCATATAGT

NMB_REF
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NMB_MUT
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Fig. 5 (cont')

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TCCCTGACTTCCTGAGGCACAGAACCAGCAGCCCCTGAGGACCTCAGATGTAAGGCCTAG

NMB_REF
GAGCTTGGGCTGGCTGAGTCTGAAGGGAAACAATGTCACCTCTAATGCCCTTGGTTTTGA 2820
NMB_MUT
GAGCTTGGGCTGGCTGAGTCTGAAGGGAAACAATGTCACCTCTAATGCCCTTGGTTTTGA

NMB_REF
AGCTCTGACACATGCAGACCAACTAGAGAATCTCAGAAGCAGCAGTGCCTACGTCTGGGG 2880
NMB_MUT
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NMB_REF
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NMB_MUT
CTTCAGAGTGAGGTCTGGGGCAGAGCTGGGGTGGGGGAGTGAGGACGCTGACACTAGCCC

NMB_REF
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NMB_MUT
AGCACCAGCACTGTATTTGGATTTTCTTCCACGATCTTCTTTGACTGTCATGACCACCC

NMB_REF
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NMB_MUT
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NMB_REF
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NMB_MUT
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NMB_REF
CACTTAGGAATGGCAGGATGCCCCTATCTTTATCAGGAGCCCCTCCCTGGCTCAATTCTT 3180
NMB_MUT
CACTTAGGAATGGCAGGATGCCCCTATCTTTATCAGGAGCCCCTCCCTGGCTCAATTCTT

NMB_REF
CTGTATGTTTCTCTTCAGTACAGGAGGCTGCTGGTACAAATACTGCAGAAATGACACCAA 3240
NMB_MUT
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Fig. 5 (cont')

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NMB_MUT
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NMB_REF
GGACCCTGTTGATGGCCCCATCTGGATGTAAATCCTGAGCTCAAATCTCTGTTACTCCAT 3360
NMB_MUT
GGACCCTGTTGATGGCCGCATCTGGATGTAAATCCTGAGCTCAAATCTCTGTTACTCCAT

NMB_REF
TACTGTGATTTCTGGCTGGGTCACCAGAAATATCGCTGATGCAGACACAGATTATGTTCC 3420
NMB_MUT
TACTGTGATTTCTGGCTGGGTCACCAGAAATATCGCTGATGCAGACACAGATTATGTTCC

NMB_REF
TGCTGTATTTCTGCTTCCCTGTTGAATTGGTGAATAAAACCTTGCTCTTTACATACAAT 3480
NMB_MUT
TGCTGTATTTCTGCTTCCCTGTTGAATTGGTGAATAAAACCTTGCTCTTTACATAAAAT

NMB_REF
GCCTGGTCCTCTCCTTTCACCCGTCTTTTAGGGGATGGGAGGAAAAGGGGGCTGGAGGGC 3540
NMB_MUT
GCCTGGTCCTCTCCTTTCACCCGTCTTTTAGGGGATGGGAGGAAAAGGGGGCTGGAGGGC

NMB_REF
AGA GTGTT CAGTGAGATGGGGCTGGCTCAAAAAGTCCAGAATACCCCATGCCATGGCACC 3600
NMB_MUT
AGA GTGTT CAGTGAGATGGGGCTGGCTCAAAAAGTCCAGAATACCCCATGCCATGGCACC

NMB_REF
AGCCTGGCACTGACTCTGGCCTCCTACCCATTCAATCAGCAAGCAAATAACGCCTGTTGC 3660
NMB_MUT
AGCCTGGCACTGACTCTGGCCTCCTACCCATTCAATCAGCAAGCAAATAACGCCTGTTGC

NMB_REF ATGCCAGGCTTCGTGCC 3677
NMB_MUT ATGCCAGGCTTCGTGCC

Fig. 5 (cont:')

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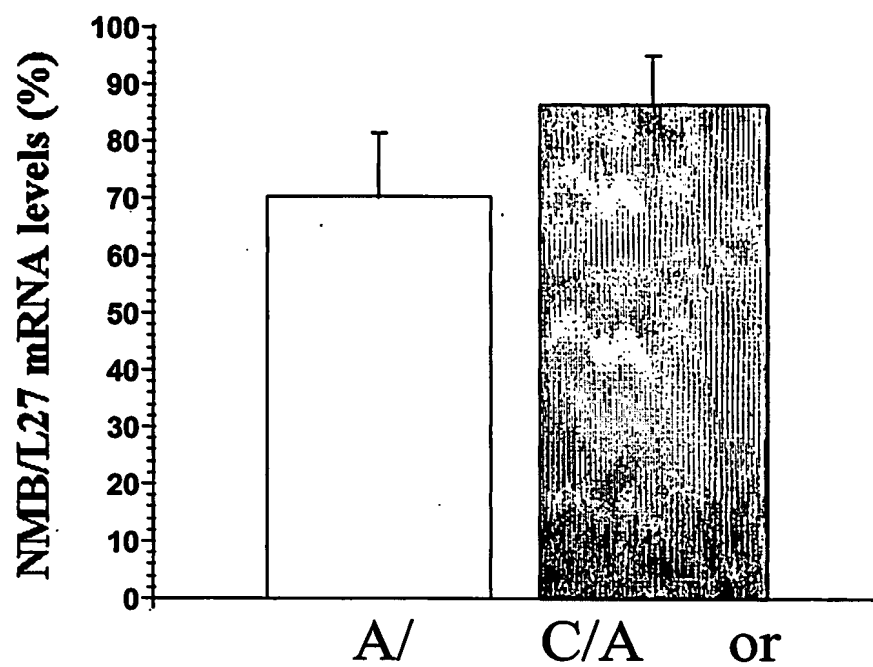


Fig. 6

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g-433 C>T or rs1849288 (within NMB promoter)

NMB_REF

CTGTTACCCGGGAGGAGAGCTCCTCGCCCGACCTCTACCTCATGAAGAGAGGCTCAGAG

NMB_MUT

CTGTTACCCGGGAGGAGAGCTCTTCGCCCGACCTCTACCTCATGAAGAGAGGCTCAGAG

g.438 C>G or IVS1+281 C>G or rs2175567 (within NMB intron 1)

NMB_REF

TTACCTTAGGCGAGACTTAACCGAATCTTCTAACCGCTGGTGTGTTTTTGCTGCACCTCC

NMB_MUT

TTACCTTAGGCGAGACTTAACCGAATCTTCTAACCGCTGGTGTGTTTTTGCTGCACCTCC

g.630 C>A or IVS1+473 C>A or rs2292462 (within NMB intron 1)

NMB_REF

GGAAAAGCTGAGGGAGCAGGCTTTGCCACCACCCAGACACCTTTGTGGCTCCTTGGTGAG

NMB_MUT

GGAAAAGCTGAGGGAGCAGGATTTGCCACCACCCAGACACCTTTGTGGCTCCTTGGTGAG

g.864 C>A or c.217 C>A (position on the coding sequence (cDNA) from the NMB first codon) or p.P73T (within NMB exon 2) or rs1051168

NMB_REF

CCAGCCCATCCCCATTGGGGACAGCTCCCCACACCTCCCTGAGGGACCAGCGACTGCAGC

NMB_MUT

CCAGCCCATCCCCATTGGGGACAGCTACCCACACCTCCCTGAGGGACCAGCGACTGCAGC

g.1043 G>A or IVS2+66 G>A (unknown in databases) (within NMB intron 2)

NMB_REF

GGCCATCCCCGGATCCTGCATGGGAGGAATTACCACCCAGTACTGTATTAGGGTGTGACT

NMB_MUT

GGCCATCCCCGGATCCTGCATGGAAGGAATTACCACCCAGTACTGTATTAGGGTGTGACT

g.1173 G>C or IVS2+196 G>C(unknown in databases) (within NMB intron 2)

NMB_REF

GCAGAGCTCAAAGGAGGAACAGTCCAAAGAAAGGAAGCTGACCTTCCCAGTAGACCCCAT

NMB_MUT

GCAGAGCTCAAAGGAGGAACAGTCCAAACAAAGGAAGCTGACCTTCCCAGTAGACCCCAT

g.2493 A>G or IVS2-251 A>G or rs3809508 (within NMB intron 2)

NMB_REF

GTGAGGACGCTGACACTAGCCCAGCACCAAGCACTGTATTTGGATTTTCTTCCACGATCT

NMB_MUT

GTGAGGACGCTGACACTAGCCCAGCACCAAGCACTGTATTTGGATTTTCTTCCACGATCT

Fig. 7

7/7

g.2708 C>T or IVS2-36 C>T (unknown in databases) (within NMB intron 2)

NMB_REF

AATGGCAGGATGCCCCTATCTTTATCAGGAGCCCCTCCCTGGCTCAATTCTTCTGTATGT

NMB_MUT

AATGGCAGGATGCCCCTATCTTTATCAGGAGCCCTCCCTGGCTCAATTCTTCTGTATGT

g.2817 T>C or g.*38 T>C or rs3748371 (within NMB 3' untranslated region)

NMB_REF

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NMB_MUT

TAATGGGGCAGACACAACAGCGTGGCTTAGACTGTGCCCACCCAGGGAAGGTGCTGAATG

g.2863 C>G or g.*84 C>G or rs1804012 (within NMB 3' untranslated region)

NMB_REF

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NMB_MUT

GTGCTGAATGGGACCCTGTTGATGGCCGCATCTGGATGTAAATCCTGAGCTCAAATCTCT

g.3022 C>A or g.*243 C>A or rs3748372 (within NMB 3' untranslated region)

NMB_REF

ATAAAACCTTGCTCTTTACATACAATGCCTGGTCCTCTCCTTTCACCCGTCTTTTAGGGG

NMB_MUT

ATAAAACCTTGCTCTTTACATAAAATGCCTGGTCCTCTCCTTTCACCCGTCTTTTAGGGG

Fig. 7 (cont')